

47 4  
0) 90  
0) 10

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/891,064A

DATE: 12/26/2001  
TIME: 11:39:22

Input Set : A:\754cip.seq.txt  
Output Set: N:\CRF3\12262001\I891064A.raw

ENTERED

5 <110> APPLICANT: James M. Anderson  
6 Christina M. Van Itallie  
8 <120> TITLE OF INVENTION: Human Occludin, Its Uses and Enhancement of Drug  
9 Absorption Using Occludin Inhibitors  
11 <130> FILE REFERENCE: OCR-754.CIP  
13 <140> CURRENT APPLICATION NUMBER: US 09/891,064A  
14 <141> CURRENT FILING DATE: 2001-06-25  
16 <150> PRIOR APPLICATION NUMBER: US 09/142,732  
17 <151> PRIOR FILING DATE: 1998-09-15  
19 <160> NUMBER OF SEQ ID NOS: 6  
20 <170> SOFTWARE: MS DOS  
22 <210> SEQ ID NO: 1  
24 <211> LENGTH: 2312  
26 <212> TYPE: DNA  
28 <213> ORGANISM: Homo sapiens  
30 <220> FEATURE:  
32 <221> NAME/KEY: mat\_peptide  
34 <222> LOCATION: complete sequence  
36 <223> OTHER INFORMATION: human occludin  
38 <400> SEQUENCE: 1  
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41 cgaacgcacc ccgggggtgt cagggacccc catccgtgct gccccctagg 100  
42 agcccgccgc tctcctctgc gccccgcctc tcggggccca acatcgcgcg 150  
43 gttccttaa cagcgcgcgtg gcagggtgtg ggaagcagga ccgcgtcc 200  
44 ccgcgcgcgc ccatcccgagt ttccaggtaa ttgggtcaccg agggaggagg 250  
45 ccgcacacacc acacccatcac tcccgcttcc acctctccct ccctgcttcc 300  
46 tcttggcgga ggcggcagga accgagagcc aggtccagag cgccgaggag 350  
47 ccggctctagg acgcagcaga ttgggttatac ttggaaagcta aagggcattg 400  
48 ctcatcctga agatcagctg accattgaca atcagccatg tcatccaggc 450  
49 ctcttggaaag tccacccct tacaggcctg atgaattcaa accgaatcat 500  
50 tatgcaccaa gcaatgacat atatggtgg aagatgcatg ttgcaccaat 550  
51 gctctctcag ccagctact ctttttaccc agaagatgaa attcttact 600  
52 tctacaaatg gacctctcct ccaggagtga ttccggatcct gtctatgctc 650  
53 attattgtga tgtgcattgc catcttgc tttgtggcct ccacgcttgc 700  
54 ctgggacaga ggctatggaa cttccctttt aggaggttagt gttaggctacc 750  
55 cttatggagg aagtggctt ggtagctacg gaagtggcta tggctatggc 800  
56 tatggttatg gctatggcta cggaggctat acagacccaa gagcagcaaa 850  
57 gggcttcatg ttggccatgg ctgcctttt tttcattgcc gcgttggta 900  
58 tctttgttac cagtgttata agatctgaaa tgtccagaac aagaagatac 950  
59 tacttaagtg tgataatagt gaggctatc ctgggcatca tgggtttat 1000  
60 tgccacaatt gtctatataa tgggagtgaa cccaaactgct cagtcttctg 1050  
61 gatctctata tggttcacaa atatatgccc tctgcaacca attttataca 1100  
62 cctgcagcta ctggactcta cgtggatcag tattttgtatc actactgtgt 1150  
63 tggatccc caggaggcca ttgcattgt actggggttc atgattattg 1200  
64 tggctttgc ttaataatt ttctttgtc tgaaaactcg aagaaagatg 1250  
65 gacaggtatg acaagtccaa tattttgtgg gacaaggaac acatttatga 1300  
66 tgagcagccc cccaaatgtcg aggagtgggt taaaaatgtg tctgcaggca 1350

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67 cacaggacgt gccttcaccc ccatctgact atgtggaaag agttgacagt 1400  
68 cccatggcat actcttccaa tggcaaagtg aatgacaagc gtttttatcc 1450  
69 agagtcttcc tataaatcca cgccggttcc tgaagtgggt caggagcttc 1500  
70 cattaaacttc gcctgtggat gacttcaggc agcctcgta cagcagcgg 1550  
71 ggttaactttg agacacacctc aaaaagagca cctgcaaagg gaagagcagg 1600  
72 aaggtacaaag agaacagagc aagatcacta tgagacagac tacacaactg 1650  
73 gcggcgagtc ctgtgatgag ctggaggagg actggatcag ggaatatcca 1700  
74 cctatcactt cagatcaaca aagacaactg tacaagagga attttgacac 1750  
75 tggcctacag gaatacaaga gcttacaatc agaacttgat gagatcaata 1800  
76 aagaactctc ccgtttggat aaagaattgg atgactatag agaagaaaagt 1850  
77 gaagagtaca tggctgctgc tgatgaatac aatagactga agcaagtgaa 1900  
78 gggatctgca gattacaaaa gtaagaagaa tcattgcaag cagttaaaga 1950  
79 gcaaattgtc acacatcaag aagatggtt gagactatga tagacagaaaa 2000  
80 acatagaagg ctgatgccaa gttgtttgag aaattaagta tctgacatct 2050  
81 ctgcaatctt ctcagaaggc aaatgacttt ggaccataac cccggaaagcc 2100  
82 aaacctctgt gagcatcaca aagttttggg ttgcttaac atcatcagta 2150  
83 ttgaagcatt ttataaatcg ctttgataa tcaactggc tgaacaactc 2200  
84 caattaagga ttttatgctt taaacattgg ttcttgatt aagaatgaaa 2250  
85 tactgttga ggttttaag ccttaaagga aggttctggt gtgaactaaa 2300  
86 cttcacacc cc 2312

89 <210> SEQ ID NO: 2

91 <211> LENGTH: 522

93 <212> TYPE: PRT

95 <213> ORGANISM: Homo sapiens

97 <220> FEATURE:

99 <221> NAME/KEY: peptide

101 <222> LOCATION: complete sequence

103 <223> OTHER INFORMATION: human occludin

105 <400> SEQUENCE: 2

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110	Glu	Phe	Lys	Pro	Asn	His	Tyr	Ala	Pro	Ser	Asn	Asp	Ile	Tyr	Gly
111					20				25				30		
113	Gly	Glu	Met	His	Val	Arg	Pro	Met	Leu	Ser	Gln	Pro	Ala	Tyr	Ser
114					35				40				45		
116	Phe	Tyr	Pro	Glu	Asp	Glu	Ile	Leu	His	Phe	Tyr	Lys	Trp	Thr	Ser
117					50				55				60		
119	Pro	Pro	Gly	Val	Ile	Arg	Ile	Leu	Ser	Met	Leu	Ile	Ile	Val	Met
120					65				70				75		
122	Cys	Ile	Ala	Ile	Phe	Ala	Cys	Val	Ala	Ser	Thr	Leu	Ala	Trp	Asp
123					80				85				90		
125	Arg	Gly	Tyr	Gly	Thr	Ser	Leu	Leu	Gly	Gly	Ser	Val	Gly	Tyr	Pro
126					95				100				105		
128	Tyr	Gly	Gly	Ser	Gly	Phe	Gly	Ser	Tyr	Gly	Ser	Gly	Tyr	Gly	Tyr
129					110				115				120		
131	Gly	Tyr	Thr	Asp	Pro	Arg									
132					125				130				135		
134	Ala	Ala	Lys	Gly	Phe	Met	Leu	Ala	Met	Ala	Ala	Phe	Cys	Phe	Ile
135					140				145				150		

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137 Ala Ala Leu Val Ile Phe Val Thr Ser Val Ile Arg Ser Glu Met  
138 155 160 165  
140 Ser Arg Thr Arg Arg Tyr Tyr Leu Ser Val Ile Ile Val Ser Ala  
141 170 175 180  
143 Ile Leu Gly Ile Met Val Phe Ile Ala Thr Ile Val Tyr Ile Met  
144 185 190 195  
146 Gly Val Asn Pro Thr Ala Gln Ser Ser Gly Ser Leu Tyr Gly Ser  
147 200 205 210  
149 Gln Ile Tyr Ala Leu Cys Asn Gln Phe Tyr Thr Pro Ala Ala Thr  
150 215 220 225  
152 Gly Leu Tyr Val Asp Gln Tyr Leu Tyr His Tyr Cys Val Val Asp  
153 230 235 240  
155 Pro Gln Glu Ala Ile Ala Ile Val Leu Gly Phe Met Ile Ile Val  
156 245 250 255  
158 Ala Phe Ala Leu Ile Ile Phe Phe Ala Val Lys Thr Arg Arg Lys  
159 260 265 270  
161 Met Asp Arg Tyr Asp Lys Ser Asn Ile Leu Trp Asp Lys Glu His  
162 275 280 285  
164 Ile Tyr Asp Glu Gln Pro Pro Asn Val Glu Glu Trp Val Lys Asn  
165 290 295 300  
167 Val Ser Ala Gly Thr Gln Asp Val Pro Ser Pro Pro Ser Asp Tyr  
168 305 310 315  
170 Val Glu Arg Val Asp Ser Pro Met Ala Tyr Ser Ser Asn Gly Lys  
171 320 325 330  
173 Val Asn Asp Lys Arg Phe Tyr Pro Glu Ser Ser Tyr Lys Ser Thr  
174 335 340 345  
176 Pro Val Pro Glu Val Val Gln Glu Leu Pro Leu Thr Ser Pro Val  
177 350 355 360  
179 Asp Asp Phe Arg Gln Pro Arg Tyr Ser Ser Gly Gly Asn Phe Glu  
180 365 370 375  
182 Thr Pro Ser Lys Arg Ala Pro Ala Lys Gly Arg Ala Gly Arg Ser  
183 380 385 390  
185 Lys Arg Thr Glu Gln Asp His Tyr Glu Thr Asp Tyr Thr Thr Gly  
186 395 400 405  
188 Gly Glu Ser Cys Asp Glu Leu Glu Glu Asp Trp Ile Arg Glu Tyr  
189 410 415 420  
191 Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln Leu Tyr Lys Arg Asn  
192 425 430 435  
194 Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu Gln Ser Glu Leu  
195 440 445 450  
197 Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys Glu Leu Asp  
198 455 460 465  
200 Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala Asp Glu  
201 470 475 480  
203 Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys Ser  
204 485 490 495  
206 Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile  
207 500 505 510  
209 Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr

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210 515 520  
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216 <211> LENGTH: 24  
218 <212> TYPE: PRT  
220 <213> ORGANISM: Artificial Sequence  
222 <220> FEATURE:  
224 <221> NAME/KEY: peptide  
226 <223> OTHER INFORMATION: construct used in experiments  
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230 Cys Asp Arg Gly Tyr Gly Thr Ser Leu Leu Gly Gly Ser Val Gly  
231 5 10 15  
233 Tyr Pro Tyr Gly Gly Ser Gly Phe Gly  
234 20  
238 <210> SEQ ID NO: 4  
240 <211> LENGTH: 24  
242 <212> TYPE: PRT  
244 <213> ORGANISM: Artificial Sequence  
246 <220> FEATURE:  
248 <221> NAME/KEY: peptide  
250 <223> OTHER INFORMATION: construct used in experiments  
252 <400> SEQUENCE: 4  
254 Cys Ser Tyr Gly Ser Gly Tyr Gly Tyr Gly Tyr Gly Tyr  
255 5 10 15  
257 Gly Tyr Gly Gly Tyr Thr Asp Pro Arg  
258 20  
262 <210> SEQ ID NO: 5  
264 <211> LENGTH: 20  
266 <212> TYPE: PRT  
268 <213> ORGANISM: Artificial Sequence  
270 <220> FEATURE:  
272 <221> NAME/KEY: peptide  
274 <223> OTHER INFORMATION: construct used in experiments  
276 <400> SEQUENCE: 5  
278 Asn His Tyr Ala Pro Ser Asn Asp Ile Tyr Gly Gly Glu Met Val  
279 5 10 15  
281 His Arg Pro Met Leu  
282 20  
286 <210> SEQ ID NO: 6  
288 <211> LENGTH: 11  
290 <212> TYPE: PRT  
292 <213> ORGANISM: Artificial Sequence  
294 <220> FEATURE:  
296 <221> NAME/KEY: peptide  
298 <223> OTHER INFORMATION: construct used in experiments  
300 <400> SEQUENCE: 6  
302 Ala Ser Gln Gln Val Tyr Arg Lys Asp Pro Cys  
303 5 10

**VERIFICATION SUMMARY**

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